SEQUENCE LISTING

<110> ROTH, RICHARD B.
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<120> METHODS FOR IDENTIFYING RISK OF BREAST CANCER AND TREATMENTS
      THEREOF

<130> SEQ-4068-UT

<140> US 10/723,518
<141> 2003-11-25

<150> US 60/429,136
<151> 2002-11-25

<150> US 60/490,234
<151> 2003-07-24

<150> US 60/504,258
<151> 2003-09-18

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gaacagtcaa tgaaggcaaa aaaaaaaaaa accaaaaaaa aaaaaaaaac acaaaacact  80040

grttaattgc tgtttcaaat ttttccattc aatttgtaaa atttcgwttt ttttttttta  80100

caaaatttcc tcttagttga cacatgctta ttatagaaaa aatgttaaaa taaaagaaac  80160

agaaagcaga aaagtaacct atgcaatgtt tagcactcag agaaaagcaa tttaaatgtt  80220

gttccacacc ctcctgaact tttattattt ttttaacata attgtgttca tattgaatat.  80280

acatttttg tattctgggt atttactcac ttaatgtgac ataggtgtgt ttgcatatta  80340

ttacatactc ttcataaaga taattcttaa caacttcaca atattctgac aagtatatgt  80400

gttcccagaa gtatgaatat tttattaatt tgacacacat taaattgata catatagaca  80460

attacctttc caagaattgt actgatttac accattatat tatgatacca ttatattgtg  80520

tgagcatgcc tatttcacca cattttcaat agcattaatc tatttctgga ctgtttattc  80580

caagatttat ctttttttcac cagttttgta aaaactatta cacactttcc ctcacattaa  80640

cattgaaatt gcttctaaat gcaattaata aaaataatat tgagattttg attgtgtctc  80700

tttccgtcaa acctttccat gacttccctt ttgtctagtt cagtggtgct cagccagggg  80760

cgattttatc ccccaggaga aattggacaa tatctggggg cattttggtt gtcccaactg  80820
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gagggtggga ctgggggagg cagggttagt ggagagtctt gctactggca tctagtgttt   80880

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caaaggattt ccccaagttt tccaaaatgt caatagtgtg ggtgggggtc aaaaaactct   81000

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gggaggacga gaaagaggta tatctttcat ctatttcaaa tcatgctatg ttgcaatgcc   81240

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cataaatcca tgtggcttca aactctttat aacaaaatga gatacagtgt gcatttaata   81360

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tacaatttcc atttgaacct gaaaactggt tcagtttaaa aaaattcccg tccatttttt   81480

tacaatcaat gaacctacat tgaaatatca ttatatgtac atatacatat aaattacatt   81540

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gctcagaaca ggaagttgtt ccaagtcaca gatctatgaa gattatagat caaaccacat   81780

tctgtgtgat gccaagaccc tatatccagc tttttctaaa tagcagtctt ttgggtttca   81840

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gaattcctgg gcttgaccta ttactgcacc tccagcatcc aagagcactg tcttacaact   82200

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atgccactta gactaattaa cacaaccttt ggtgtagata ccaataagaa tagtttaagt   82320

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agaattatct ttccagtgtt acttataata ataacaaaat ttattgaaat gtctaagacg   82620

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tttagaaccc ttggtgtctc ccaagtacat gccagtagta gctccctttt ctcagtagtg   82800

ccaatacaaa atgtctttag acatcgtcaa atgtccctg ggggcaaaat tgcacctagt    82860

tgagacctat aaaatggact acaacccatg tagctattaa gagtatgtta aaaaaatatt   82920

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taatttccat aataaccctc agaggttggt aattaacccc atttgataaa taaggaaaca   83160

gaatctcaga caggttaagc agctgaatga taattttata atattaaccg cagtcatgtc   83220

tgggtagtga aattgggtgt aattatttat ctctgtattt tccaagattt caacaataag   83280

catctattat ttttaatcag aaaacttaac aaatgacatt attgggccyg gcacagtggc   83340

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<213> Homo sapiens

<220>
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<222> (1)..(1893)

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att tgg cta gcg gcc cat tgg gat aag aag cta acc aaa gcc cat gtg   96
Ile Trp Leu Ala Ala His Trp Asp Lys Lys Leu Thr Lys Ala His Val
            20                  25                  30

ttc gag tgt aat tta gag agc agc gtg gag agt atc atc tca cca aag   144
Phe Glu Cys Asn Leu Glu Ser Ser Val Glu Ser Ile Ile Ser Pro Lys
        35                  40                  45
```

```
gtg aaa atg gca tta cgg aca tca gga cat ctc tta ctg gga gta gtt    192
Val Lys Met Ala Leu Arg Thr Ser Gly His Leu Leu Leu Gly Val Val
    50                  55                  60

cga atc tat cac agg aaa gcc aaa tac ctt ctt gca gac tgt aat gaa    240
Arg Ile Tyr His Arg Lys Ala Lys Tyr Leu Leu Ala Asp Cys Asn Glu
65                  70                  75                  80

gca ttc att aag ata aag atg gct ttt cgg cca ggt gtg gtt gac ctg    288
Ala Phe Ile Lys Ile Lys Met Ala Phe Arg Pro Gly Val Val Asp Leu
                85                  90                  95

cct gag gaa aat cgg gaa gca gct tat aat gcc att act tta cct gaa    336
Pro Glu Glu Asn Arg Glu Ala Ala Tyr Asn Ala Ile Thr Leu Pro Glu
                100                 105                 110

gaa ttt cat gac ttt gat cag cca ctg cct gac tta gat gac atc gat    384
Glu Phe His Asp Phe Asp Gln Pro Leu Pro Asp Leu Asp Asp Ile Asp
            115                 120                 125

gtg gcc cag cag ttc agc ttg aat cag agt aga gtg gaa gag ata acc    432
Val Ala Gln Gln Phe Ser Leu Asn Gln Ser Arg Val Glu Glu Ile Thr
    130                 135                 140

atg aga gaa gaa gtt ggg aac atc agt att tta caa gaa aat gat ttt    480
Met Arg Glu Glu Val Gly Asn Ile Ser Ile Leu Gln Glu Asn Asp Phe
145                 150                 155                 160

ggt gat ttt gga atg gat gat cgt gag ata atg aga gaa ggc agt gct    528
Gly Asp Phe Gly Met Asp Asp Arg Glu Ile Met Arg Glu Gly Ser Ala
                165                 170                 175

ttt gag gat gac gac atg tta gta agc act act act tct aac ctc cta    576
Phe Glu Asp Asp Asp Met Leu Val Ser Thr Thr Thr Ser Asn Leu Leu
            180                 185                 190

tta gag tct gaa cag agc acc agc aat ctg aat gag aaa att aac cat    624
Leu Glu Ser Glu Gln Ser Thr Ser Asn Leu Asn Glu Lys Ile Asn His
        195                 200                 205

tta gaa tat gaa gat caa tat aag gat gat aat ttt gga gaa gga aat    672
Leu Glu Tyr Glu Asp Gln Tyr Lys Asp Asp Asn Phe Gly Glu Gly Asn
        210                 215                 220

gat ggt gga ata tta gat gac aaa ctt att agt aat aat gat ggc ggt    720
Asp Gly Gly Ile Leu Asp Asp Lys Leu Ile Ser Asn Asn Asp Gly Gly
225                 230                 235                 240

atc ttt gat gat ccc cct gcc ctc tct gag gca ggg gtg atg ttg cca    768
Ile Phe Asp Asp Pro Pro Ala Leu Ser Glu Ala Gly Val Met Leu Pro
                245                 250                 255

gag cag cct gca cat gac gat atg gat gag gat gat aat gta tca atg    816
Glu Gln Pro Ala His Asp Asp Met Asp Glu Asp Asp Asn Val Ser Met
                260                 265                 270
```

```
ggt ggg cct gat agt cct gat tca gtg gat ccc gtt gaa cca atg cca    864
Gly Gly Pro Asp Ser Pro Asp Ser Val Asp Pro Val Glu Pro Met Pro
        275             280             285

acc atg act gat caa aca aca ctt gtt cca aat gag gaa gaa gca ttt    912
Thr Met Thr Asp Gln Thr Thr Leu Val Pro Asn Glu Glu Glu Ala Phe
        290             295             300

gca ttg gag cct att gat ata act gtt aaa gaa aca aaa gcc aag agg    960
Ala Leu Glu Pro Ile Asp Ile Thr Val Lys Glu Thr Lys Ala Lys Arg
305             310             315             320

aag agg aag cta att gtt gac agt gtc aaa gag ttg gat agc aag aca   1008
Lys Arg Lys Leu Ile Val Asp Ser Val Lys Glu Leu Asp Ser Lys Thr
            325             330             335

att aga gcc caa ctt agt gat tat tca gat att gtt act act ttg gat   1056
Ile Arg Ala Gln Leu Ser Asp Tyr Ser Asp Ile Val Thr Thr Leu Asp
            340             345             350

ctg gca ccg ccc acc aag aaa ttg atg atg tgg aaa gag aca gga gga   1104
Leu Ala Pro Pro Thr Lys Lys Leu Met Met Trp Lys Glu Thr Gly Gly
            355             360             365

gta gaa aaa ctg ttt tct tta cct gct cag cct ttg tgg aat aac aga   1152
Val Glu Lys Leu Phe Ser Leu Pro Ala Gln Pro Leu Trp Asn Asn Arg
        370             375             380

cta ctg aag ctc ttt aca cgc tgt ctt aca ccg ctt gta cca gaa gac   1200
Leu Leu Lys Leu Phe Thr Arg Cys Leu Thr Pro Leu Val Pro Glu Asp
385             390             395             400

ctt aga aaa agg agg aaa gga gga gag gca gat aat ttg gat gaa ttc   1248
Leu Arg Lys Arg Arg Lys Gly Gly Glu Ala Asp Asn Leu Asp Glu Phe
            405             410             415

ctc aaa gaa ttt gaa aat cca gag gtt cct aga gag gac cag caa cag   1296
Leu Lys Glu Phe Glu Asn Pro Glu Val Pro Arg Glu Asp Gln Gln Gln
            420             425             430

cag cat cag cag cgt gat gtt atc gat gag ccc att att gaa gag cca   1344
Gln His Gln Gln Arg Asp Val Ile Asp Glu Pro Ile Ile Glu Glu Pro
            435             440             445

agc cgc ctc cag gag tca gtg atg gag gcc agc aga aca aac ata gat   1392
Ser Arg Leu Gln Glu Ser Val Met Glu Ala Ser Arg Thr Asn Ile Asp
            450             455             460

gag tca gct atg cct cca cca cca cct cag gga gtt aag cga aaa gct   1440
Glu Ser Ala Met Pro Pro Pro Pro Pro Gln Gly Val Lys Arg Lys Ala
465             470             475             480

gga caa att gac cca gag cct gtg atg cct cct cag cag gta gag cag   1488
Gly Gln Ile Asp Pro Glu Pro Val Met Pro Pro Gln Gln Val Glu Gln
            485             490             495
```

```
atg gaa ata cca cct gta gag ctt ccc cca gaa gaa cct cca aat atc    1536
Met Glu Ile Pro Pro Val Glu Leu Pro Pro Glu Glu Pro Pro Asn Ile
            500             505             510

tgt cag cta ata cca gag tta gaa ctt ctg cca gaa aaa gag aag gag    1584
Cys Gln Leu Ile Pro Glu Leu Glu Leu Leu Pro Glu Lys Glu Lys Glu
            515             520             525

aaa gag aag gaa aaa gaa gat gat gaa gag gaa gag gat gaa gat gca    1632
Lys Glu Lys Glu Lys Glu Asp Asp Glu Glu Glu Glu Asp Glu Asp Ala
            530             535             540

tca ggg ggc gat caa gat cag gaa gaa aga aga tgg aac aaa agg act    1680
Ser Gly Gly Asp Gln Asp Gln Glu Glu Arg Arg Trp Asn Lys Arg Thr
545             550             555             560

cag cag atg ctt cat ggt ctt cag cgt gct ctt gct aaa act gga gct    1728
Gln Gln Met Leu His Gly Leu Gln Arg Ala Leu Ala Lys Thr Gly Ala
                565             570             575

gaa tct atc agt ttg ctt gag tta tgt cga aat acg aac aga aaa caa    1776
Glu Ser Ile Ser Leu Leu Glu Leu Cys Arg Asn Thr Asn Arg Lys Gln
                580             585             590

gct gcc gca aag ttc tac agc ttc ttg gtt ctt aaa aag cag caa gct    1824
Ala Ala Ala Lys Phe Tyr Ser Phe Leu Val Leu Lys Lys Gln Gln Ala
                595             600             605

att gag ctg aca cag gaa gaa ccg tac agt gac atc atc gca aca cct    1872
Ile Glu Leu Thr Gln Glu Glu Pro Tyr Ser Asp Ile Ile Ala Thr Pro
            610             615             620

gga cca agg ttc cat att ata taa                                    1896
Gly Pro Arg Phe His Ile Ile
625             630
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<212> PRT
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Ile Trp Leu Ala Ala His Trp Asp Lys Lys Leu Thr Lys Ala His Val
            20                  25                  30

Phe Glu Cys Asn Leu Glu Ser Ser Val Glu Ser Ile Ile Ser Pro Lys
            35                  40                  45

Val Lys Met Ala Leu Arg Thr Ser Gly His Leu Leu Leu Gly Val Val
        50                  55                  60

Arg Ile Tyr His Arg Lys Ala Lys Tyr Leu Leu Ala Asp Cys Asn Glu
65                  70                  75                  80
```

```
Ala Phe Ile Lys Ile Lys Met Ala Phe Arg Pro Gly Val Val Asp Leu
                85                  90                      95

Pro Glu Glu Asn Arg Glu Ala Ala Tyr Asn Ala Ile Thr Leu Pro Glu
            100                 105             110

Glu Phe His Asp Phe Asp Gln Pro Leu Pro Asp Leu Asp Asp Ile Asp
        115             120             125

Val Ala Gln Gln Phe Ser Leu Asn Gln Ser Arg Val Glu Glu Ile Thr
    130             135             140

Met Arg Glu Glu Val Gly Asn Ile Ser Ile Leu Gln Glu Asn Asp Phe
145             150             155             160

Gly Asp Phe Gly Met Asp Asp Arg Glu Ile Met Arg Glu Gly Ser Ala
            165             170             175

Phe Glu Asp Asp Asp Met Leu Val Ser Thr Thr Thr Ser Asn Leu Leu
            180             185             190

Leu Glu Ser Glu Gln Ser Thr Ser Asn Leu Asn Glu Lys Ile Asn His
        195             200             205

Leu Glu Tyr Glu Asp Gln Tyr Lys Asp Asp Asn Phe Gly Glu Gly Asn
    210             215             220

Asp Gly Gly Ile Leu Asp Asp Lys Leu Ile Ser Asn Asn Asp Gly Gly
225             230             235             240

Ile Phe Asp Asp Pro Pro Ala Leu Ser Glu Ala Gly Val Met Leu Pro
            245             250             255

Glu Gln Pro Ala His Asp Asp Met Asp Glu Asp Asp Asn Val Ser Met
            260             265             270

Gly Gly Pro Asp Ser Pro Asp Ser Val Asp Pro Val Glu Pro Met Pro
        275             280             285

Thr Met Thr Asp Gln Thr Thr Leu Val Pro Asn Glu Glu Glu Ala Phe
    290             295             300

Ala Leu Glu Pro Ile Asp Ile Thr Val Lys Glu Thr Lys Ala Lys Arg
305             310             315             320

Lys Arg Lys Leu Ile Val Asp Ser Val Lys Glu Leu Asp Ser Lys Thr
            325             330             335

Ile Arg Ala Gln Leu Ser Asp Tyr Ser Asp Ile Val Thr Thr Leu Asp
        340             345             350

Leu Ala Pro Pro Thr Lys Lys Leu Met Met Trp Lys Glu Thr Gly Gly
        355             360             365

Val Glu Lys Leu Phe Ser Leu Pro Ala Gln Pro Leu Trp Asn Asn Arg
    370             375             380
```

```
Leu Leu Lys Leu Phe Thr Arg Cys Leu Thr Pro Leu Val Pro Glu Asp
385             390             395                 400

Leu Arg Lys Arg Arg Lys Gly Gly Glu Ala Asp Asn Leu Asp Glu Phe
            405             410                 415

Leu Lys Glu Phe Glu Asn Pro Glu Val Pro Arg Glu Asp Gln Gln Gln
            420             425                 430

Gln His Gln Gln Arg Asp Val Ile Asp Glu Pro Ile Ile Glu Glu Pro
        435             440                 445

Ser Arg Leu Gln Glu Ser Val Met Glu Ala Ser Arg Thr Asn Ile Asp
    450             455             460

Glu Ser Ala Met Pro Pro Pro Pro Pro Gln Gly Val Lys Arg Lys Ala
465             470             475                 480

Gly Gln Ile Asp Pro Glu Pro Val Met Pro Pro Gln Gln Val Glu Gln
            485             490                 495

Met Glu Ile Pro Pro Val Glu Leu Pro Pro Glu Glu Pro Pro Asn Ile
            500             505             510

Cys Gln Leu Ile Pro Glu Leu Glu Leu Leu Pro Glu Lys Glu Lys Glu
        515             520             525

Lys Glu Lys Glu Lys Glu Asp Asp Glu Glu Glu Glu Asp Glu Asp Ala
    530             535             540

Ser Gly Gly Asp Gln Asp Gln Glu Glu Arg Arg Trp Asn Lys Arg Thr
545             550             555                 560

Gln Gln Met Leu His Gly Leu Gln Arg Ala Leu Ala Lys Thr Gly Ala
            565             570                 575

Glu Ser Ile Ser Leu Leu Glu Leu Cys Arg Asn Thr Asn Arg Lys Gln
            580             585             590

Ala Ala Ala Lys Phe Tyr Ser Phe Leu Val Leu Lys Lys Gln Gln Ala
        595             600             605

Ile Glu Leu Thr Gln Glu Glu Pro Tyr Ser Asp Ile Ile Ala Thr Pro
    610             615             620

Gly Pro Arg Phe His Ile Ile
625             630
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<210> 5
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<210> 6
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<220>
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<400> 6
ctgtggcgta cacatgaaac tg                                     22

<210> 7
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<220>
<223> Primer

<400> 7
acgttggatg acaaacgggg aaaactcctt                             30

<210> 8
<211> 35
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<220>
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acgttggatg aatgattcag tttcttcaga gtggt                       35

<210> 9
<211> 34
<212> DNA
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<220>
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<210> 10
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<220>
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<400> 10
acgttggatg tgacctttct aaaatcaaac attca                             35

<210> 11
<211> 30
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<220>
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<400> 11
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<210> 12
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<220>
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<400> 12
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<220>
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<211> 30
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<220>
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<210> 17
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<400> 17
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<210> 18
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<400> 18
acgttggatg tacttacagg catcacaggc                                    30


<210> 19
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<212> DNA
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<220>
<223> Primer

<400> 19
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<400> 23
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<210> 24
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<220>
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